RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10 038,722 A

Source: IFW 16

Date Processed by STIC: 3-24-05

ENTERED

RAW SEQUENCE LISTING   DATE: 03/24/2005
PATENT APPLICATION: US/10/038,722A   TIME: 14:43:31

Input Set : A:\D0617.70005US01 seq.txt
Output Set: N:\CRF4\03242005\J038722A.raw

```
 4 <110> APPLICANT: LEY, Arthur C.
 5        GUTERMAN, Sonia K.
 6        MARKLAND, William
 7        KENT, Rachel B.
 8        ROBERTS, Bruce L.
 9        LADNER, Robert C.
11 <120> TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS HNE INHIBITORS
13 <130> FILE REFERENCE: D0617.7005US01
15 <140> CURRENT APPLICATION NUMBER: 10/038,722A
16 <141> CURRENT FILING DATE: 2002-01-08
18 <150> PRIOR APPLICATION NUMBER: US 08/849,406
19 <151> PRIOR FILING DATE: 1999-07-21
21 <150> PRIOR APPLICATION NUMBER: PCT/US95/16349
22 <151> PRIOR FILING DATE: 1995-12-15
24 <150> PRIOR APPLICATION NUMBER: US 08/358,160
25 <151> PRIOR FILING DATE: 1994-12-16
27 <150> PRIOR APPLICATION NUMBER: US 08/133,031
28 <151> PRIOR FILING DATE: 1992-02-28
30 <160> NUMBER OF SEQ ID NOS: 140
32 <170> SOFTWARE: PatentIn version 3.1
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36 <211> LENGTH: 276
37 <212> TYPE: DNA
38 <213> ORGANISM: Artificial Sequence
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42 <223> OTHER INFORMATION: IIIsp::bpti::matureIII (initial fragment)
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47 gatttctgtc tcgagccacc atacactggg ccctgcaaag cgcgcatcat ccgctatttc    120
49 tacaatgcta aagcaggcct gtgccagacc tttgtatacg gtggttgccg tgctaagcgt    180
51 aacaacttta aatcggccga agattgcatg cgtacctgcg gtggcgccgc tgaaactgtt    240
53 gaaagttgtt tagcaaaacc ccatacagaa aattca                              276
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57 <211> LENGTH: 92
58 <212> TYPE: PRT
59 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
63 <223> OTHER INFORMATION: IIIsp::bpti::matureIII (initial fragment)
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70 Gly Ala Arg Pro Asp Phe Cys Leu Glu Pro Pro Tyr Thr Gly Pro Cys
71             20                  25                  30
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73 Lys Ala Arg Ile Ile Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys
74          35                  40                  45
76 Gln Thr Phe Val Tyr Gly Gly Cys Arg Ala Lys Arg Asn Asn Phe Lys
77     50                  55                  60
79 Ser Ala Glu Asp Cys Met Arg Thr Cys Gly Gly Ala Ala Glu Thr Val
80 65                  70                  75                  80
82 Glu Ser Cys Leu Ala Lys Pro His Thr Glu Asn Ser
83                  85                  90
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87 <211> LENGTH: 285
88 <212> TYPE: DNA
89 <213> ORGANISM: Artificial Sequence
91 <220> FEATURE:
93 <223> OTHER INFORMATION: IIIsp::itiD1::mature III fusion gene
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98 gactcttgcc agctgggcta ctcggccggt ccctgcatgg gaatgaccag caggtatttc   120
100 tataatggta catccatggc ctgtgagact ttccagtacg gcggctgcat gggcaacggt   180
102 aacaacttcg tcacagaaaa ggagtgtctg cagacctgcc gaactgtggg cgccgctgaa   240
104 actgttgaaa gttgtttagc aaaaccccat acagaaaatt cattt                   285
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108 <211> LENGTH: 95
109 <212> TYPE: PRT
110 <213> ORGANISM: Artificial Sequence
112 <220> FEATURE:
114 <223> OTHER INFORMATION: IIIsp::itiD1::mature III fusion gene
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118 Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser
119 1              5                  10                  15
122 Gly Ala Lys Glu Asp Ser Cys Gln Leu Gly Tyr Ser Ala Gly Pro Cys
123              20                  25                  30
125 Met Gly Met Thr Ser Arg Tyr Phe Tyr Asn Gly Thr Ser Met Ala Cys
126          35                  40                  45
128 Glu Thr Phe Gln Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Val
129     50                  55                  60
131 Thr Glu Lys Glu Cys Leu Gln Thr Cys Arg Thr Val Gly Ala Ala Glu
132 65                  70                  75                  80
134 Thr Val Glu Ser Cys Leu Ala Lys Pro His Thr Glu Asn Ser Phe
135                  85                  90                  95
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139 <211> LENGTH: 58
140 <212> TYPE: PRT
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
145 <223> OTHER INFORMATION: Consensus Kunitz domain
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153              20              25              30
155 Phe Ile Tyr Gly Gly Cys Gly Gly Asn Ala Asn Asn Phe Lys Thr Glu
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159    50              55
162 <210> SEQ ID NO: 6
163 <211> LENGTH: 58
164 <212> TYPE: PRT
165 <213> ORGANISM: Bos Taurus
167 <400> SEQUENCE: 6
169 Arg Pro Asp Phe Cys Leu Glu Pro Pro Tyr Thr Gly Pro Cys Lys Ala
170 1           5              10              15
172 Arg Ile Ile Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
173          20              25              30
175 Phe Val Tyr Gly Gly Cys Arg Ala Lys Arg Asn Asn Phe Lys Ser Ala
176          35              40              45
178 Glu Asp Cys Met Arg Thr Cys Gly Gly Ala
179    50              55
182 <210> SEQ ID NO: 7
183 <211> LENGTH: 58
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185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
189 <223> OTHER INFORMATION: Epi-HNE-1
191 <400> SEQUENCE: 7
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196 Phe Phe Pro Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
197          20              25              30
199 Phe Val Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Lys Ser Ala
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203    50              55
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207 <211> LENGTH: 62
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213 <223> OTHER INFORMATION: Epi-HNE-2
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218 1           5              10              15
220 Pro Cys Ile Ala Phe Phe Pro Arg Tyr Phe Tyr Asn Ala Lys Ala Gly
221          20              25              30
223 Leu Cys Gln Thr Phe Val Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn
224          35              40              45
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227    50              55              60
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233 <213> ORGANISM: Artificial Sequence
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237 <223> OTHER INFORMATION: EpiNE7
239 <400> SEQUENCE: 9
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242 1               5                   10                  15
243 Met Phe Pro Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
244             20                  25              30
246 Phe Val Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Lys Ser Ala
247         35                  40                  45
249 Glu Asp Cys Met Arg Thr Cys Gly Gly Ala
250     50                  55
253 <210> SEQ ID NO: 10
254 <211> LENGTH: 58
255 <212> TYPE: PRT
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
260 <223> OTHER INFORMATION: EpiNE3
262 <400> SEQUENCE: 10
264 Arg Pro Asp Phe Cys Leu Glu Pro Pro Tyr Thr Gly Pro Cys Val Gly
265 1               5                   10                  15
267 Phe Phe Ser Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
268             20                  25              30
270 Phe Val Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Lys Ser Ala
271         35                  40                  45
273 Glu Asp Cys Met Arg Thr Cys Gly Gly Ala
274     50                  55
277 <210> SEQ ID NO: 11
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279 <212> TYPE: PRT
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
284 <223> OTHER INFORMATION: EpiNE6
286 <400> SEQUENCE: 11
288 Arg Pro Asp Phe Cys Leu Glu Pro Pro Tyr Thr Gly Pro Cys Val Gly
289 1               5                   10                  15
291 Phe Phe Gln Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
292             20                  25              30
294 Phe Val Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Lys Ser Ala
295         35                  40                  45
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298     50                  55
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303 <212> TYPE: PRT
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308 <223> OTHER INFORMATION: EpiNE4
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313 1               5                   10              15
315 Ile Phe Pro Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
316             20                  25              30
318 Phe Val Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Lys Ser Ala
319         35                  40                  45
321 Glu Asp Cys Met Arg Thr Cys Gly Gly Ala
322     50                  55
325 <210> SEQ ID NO: 13
326 <211> LENGTH: 58
327 <212> TYPE: PRT
328 <213> ORGANISM: Artificial Sequence
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332 <223> OTHER INFORMATION: EpiNE8
334 <400> SEQUENCE: 13
336 Arg Pro Asp Phe Cys Leu Glu Pro Pro Tyr Thr Gly Pro Cys Val Ala
337 1               5                   10              15
339 Phe Phe Lys Arg Ser Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
340             20                  25              30
342 Phe Val Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Lys Ser Ala
343         35                  40                  45
345 Glu Asp Cys Met Arg Thr Cys Gly Gly Ala
346     50                  55
349 <210> SEQ ID NO: 14
350 <211> LENGTH: 58
351 <212> TYPE: PRT
352 <213> ORGANISM: Artificial Sequence
354 <220> FEATURE:
356 <223> OTHER INFORMATION: EpiNE5
358 <400> SEQUENCE: 14
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361 1               5                   10              15
363 Phe Phe Gln Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
364             20                  25              30
365 Phe Val Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Lys Ser Ala
366         35                  40                  45
368 Glu Asp Cys Met Arg Thr Cys Gly Gly Ala
369     50                  55
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375 <213> ORGANISM: Artificial Sequence
377 <220> FEATURE:
379 <223> OTHER INFORMATION: EpiNE2
381 <400> SEQUENCE: 15
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384 1               5                   10              15
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/24/2005
PATENT APPLICATION: US/10/038,722A   TIME: 14:43:32

Input Set : A:\D0617.70005US01 seq.txt
Output Set: N:\CRF4\03242005\J038722A.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:82; N Pos. 37,38,40,41,42,47,52,56,58,64,65,66,71,72,100,101,103,104
Seq#:82; N Pos. 109,110,124,125,128,133,134
Seq#:83; Xaa Pos. 13,14,16,18,19,20,22,24,34,35,37,42,43,45
Seq#:84; N Pos. 34,35,37,38,39,43,44,49,53,55,56,61,62,63,68,69,97,98,100
Seq#:84; N Pos. 101,106,107,121,122,125,130,131
Seq#:85; Xaa Pos. 12,13,15,17,18,19,21,23,33,34,36,41,42,44
Seq#:86; Xaa Pos. 2,3,4,5,6,7,9,11,12,13,14,15,16,17,18,19,20,21,22,23,24
Seq#:86; Xaa Pos. 25,27,28,30,31,32,35,36,37,38,39,40,41,42,43,44,45,46,48
Seq#:86; Xaa Pos. 49,50
Seq#:103; Xaa Pos. 1
Seq#:104; Xaa Pos. 1
Seq#:106; Xaa Pos. 1
Seq#:109; Xaa Pos. 1
Seq#:119; Xaa Pos. 14
Seq#:123; Xaa Pos. 1
Seq#:127; N Pos. 4,5,6,7,8
Seq#:128; N Pos. 4,5,6,7,8,9,10,11,12

VERIFICATION SUMMARY   DATE: 03/24/2005
PATENT APPLICATION: US/10/038,722A   TIME: 14:43:32

Input Set : A:\D0617.70005US01 seq.txt
Output Set: N:\CRF4\03242005\J038722A.raw

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L:2804 M:283 W: Missing Blank Line separator, <220> field identifier
L:2920 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:0
M:341 Repeated in SeqNo=82
L:2987 M:283 W: Missing Blank Line separator, <220> field identifier
L:3009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0
M:341 Repeated in SeqNo=83
L:3162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84 after pos.:0
M:341 Repeated in SeqNo=84
L:3253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:0
M:341 Repeated in SeqNo=85
L:3312 M:283 W: Missing Blank Line separator, <220> field identifier
L:3351 M:283 W: Missing Blank Line separator, <400> field identifier
L:3353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:0
M:341 Repeated in SeqNo=86
L:3738 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103 after pos.:0
L:3763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:104 after pos.:0
L:3808 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:106 after pos.:0
L:3873 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109 after pos.:0
L:4079 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:119 after pos.:0
L:4172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:123 after pos.:0
L:4268 M:283 W: Missing Blank Line separator, <400> field identifier
L:4269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:127 after pos.:0
L:4287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:128 after pos.:0
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